<u>Amendments to the Specification</u>:

Please replace paragraph [0038] with the following amended paragraph:

0038. In one embodiment, a T1R polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates plasma membrane trafficking, or maturation and targeting through the secretory pathway. The optional heterologous sequence may be a rhodopsin sequence, such as an N-terminal fragment of a rhodopsin. Such chimeric TlR receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a G protein, *e.g.*, $G_{\alpha15}$ or $G_{\alpha16}$ or another type of promiscuous G protein capable of pairing a wide range of chemosensory GPCRs to an intracellular signaling pathway or to a signaling protein such as phospholipase C. Alternatively, the cells may express a chimeric or variant G protein that is selected based on its ability to couple with TlRs to produce a functional TlR taste receptor. Examples of variant G proteins which are especially preferred include the G protein variants disclosed in U.S. Serial No. 09/984,292, filed on October 29, 2001, incorporated by reference herein in its entirety and the chimeric $G_{\alpha15}$ variants disclosed in U.S. Provisional Application No. ~~60/________,~~ <u>60/243,770</u> ~~Attorney Docket No. 078003-0280737~~ also incorporated by reference in its entirety. These applications disclose G protein variants that have been shown to couple better with TlRs than $G_{\alpha15}$, a well known promiscuous G protein.

Activation of such chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell. If preferred host cells do not express an appropriate G protein, they may be transfected with a gene encoding a promiscuous G protein such as those described in US Application Serial No. 60/243,770, which is herein incorporated by reference in its entirety.

Please replace paragraph [0056] with the following amended paragraph:

[0056] A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et *al., Nuc. Acids* Res. 25:3389-3402 (1977) and Altschul et *al., J Mol. Biol.* 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nim.nih.gov/)~~. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et *al.* Altschul et *al., Nuc. Acids* Res. 25:3389-3402 (1977) and Altschul et al, *J Mol Biol.* 215:403-410 (1990)). These initial neighborhood word hits act as seeds for

initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. *Natl. Acad Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Please replace paragraph [0122] with the following amended paragraph:

[0122] A chimeric nucleic acid sequence may encode a T1R ligand-binding domain within any 7-transmembrane polypeptide. Because 7-transmembrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains (e.g., extracellular domain, TM domains, cytoplasmic domain, etc.) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. Periodicity detection enhancement and alpha helical periodicity index can be done as by, e.g., Donnelly, Protein Sci. 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, see, e.g., Peitsch, Receptors *Channels 4*:161-164 (1996); Kyte & Doolittle, *J. Md. Bio.,* 157:105-132 (1982); Cronet, Protein *Eng. 6*:59-64 (1993) (homology and "discover modeling"); ~~hftp://bioinfo.weizmann.ac.il/~~.